RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/542, 769 A _____

Source: _____ PCT _____

Date Processed by STIC: _____ 03/20/2006 _____

ENTERED

PCT

```
 3 <110> APPLICANT: BUTZKE, DANIEL
 4        GOEDERT, SIGRID
 5        DITTRICH, MICHAEL
 6        RUDEL, THOMAS
 7        MEYER, THOMAS
 9 <120> TITLE OF INVENTION: L-AMINO ACID OXIDASE WITH CYTOTOXIC ACTIVITY FROM
10        APLYSIA PUNCTATA
12 <130> FILE REFERENCE: WEICKM-0046
14 <140> CURRENT APPLICATION NUMBER: 10/542,769A
15 <141> CURRENT FILING DATE: 2005 07-20
17 <150> PRIOR APPLICATION NUMBER: PCT/EP04/00423
18 <151> PRIOR FILING DATE: 2004-01-20
20 <150> PRIOR APPLICATION NUMBER: EP 03001232.2
21 <151> PRIOR FILING DATE: 2003-01-20
23 <150> PRIOR APPLICATION NUMBER: EP 03026613.4
24 <151> PRIOR FILING DATE: 2003-11-19
26 <160> NUMBER OF SEQ ID NOS: 78
28 <170> SOFTWARE: PatentIn Ver. 3.3
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1608
32 <212> TYPE: DNA
33 <213> ORGANISM: Aplysia punctata
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)..(1608)
39 <400> SEQUENCE: 1
40 atg tcg tct gct gtg ctt ctc ctg gct tgt gcg ttg gtc atc tct gtc    48
41 Met Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val
42  1               5                  10                  15
44 cac gcc gac ggt atc tgc aga aac aga cgt caa tgt aac aga gag gtg    96
45 His Ala Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val
46             20                  25                  30
48 tgc ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga   144
49 Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly
50          35                  40                  45
52 gct aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg   192
53 Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
54       50                  55                  60
56 ttc gag tac tcg gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg   240
57 Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu
58  65                  70                  75                  80
60 ccc aac aca ccc gac gtt aac ctg gag att ggc ggc atg agg ttc atc   288
61 Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile
```

(pg-6)

```
62                  85                  90                  95
64 gaa ggc gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta   336
65 Glu Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu
66                  100                 105                 110
68 acc ccc aag gtg ttc aag gaa ggt ttc ggc aag gag ggc aga caa aga   384
69 Thr Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg
70             115                 120                 125
72 ttt tac ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg   432
73 Phe Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly
74      130                 135                 140
76 gac gta ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat   480
77 Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn
78 145                 150                 155                 160
80 ctg gtc gaa tac tac ctg gag aaa ctg aca ggt cta caa ctc aac ggc   528
81 Leu Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly
82                  165                 170                 175
84 gag ccg ctc aaa cgt gag gtt gcg ctt aaa cta acc gtg ccg gac ggc   576
85 Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
86             180                 185                 190
88 aga ttc ctc tat gac ctc tcg ttt gac gaa gcc atg gat ctg gtt gcc   624
89 Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
90             195                 200                 205
92 tcc cct gag ggc aaa gag ttc acc cga gac acg cac gtc ttc aca gga   672
93 Ser Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly
94      210                 215                 220
96 gag gtc acc ctg gac gcg tcg gct gtc tcc ctc ttc gac gac cac ctg   720
97 Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
98 225                 230                 235                 240
100 gga gag gac tac tat ggc agt gag atc tac acc cta aag gaa gga ctg  768
101 Gly Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu
102             245                 250                 255
104 tct tcc gtc cca caa ggg ctc cta cag gct ttt ctg gac gcc gca gac  816
105 Ser Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp
106             260                 265                 270
108 tcc aac gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag  864
109 Ser Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys
110             275                 280                 285
112 acc aac ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat  912
113 Thr Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp
114      290                 295                 300
116 gga caa acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca  960
117 Gly Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala
118 305                 310                 315                 320
120 caa aga gtc atc ctg gcc atg ccg gta tac gct ctg aac caa cta gac  1008
121 Gln Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp
122             325                 330                 335
124 tgg aat cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtt  1056
125 Trp Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val
126             340                 345                 350
```

```
128 cgc ccg att cct gca agt aag gtg ttc atg tcc ttt gat cag ccc tgg   1104
129 Arg Pro Ile Pro Ala Ser Lys Val Phe Met Ser Phe Asp Gln Pro Trp
130         355                 360                 365
132 tgg ttg gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt   1152
133 Trp Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu
134         370                 375                 380
136 ttc agc caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac   1200
137 Phe Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr
138 385                 390                 395                 400
140 atc ctg atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg   1248
141 Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg
142                 405                 410                 415
144 gag ctg aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac   1296
145 Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr
146         420                 425                 430
148 aac cag gtt acc gaa ccc ctc aag gac acc att ctt gac cac ctc act   1344
149 Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr
150         435                 440                 445
152 gag gct tac ggc gtg gag cga gac tcg atc ccg gaa ccc gtg acc gcc   1392
153 Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala
154         450                 455                 460
156 gct tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc   1440
157 Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr
158 465                 470                 475                 480
160 tgg agg gcc ggc ttc cat ttc gat gac gtc atc agc acc atg cgt cgc   1488
161 Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg
162                 485                 490                 495
164 ccg tca ctg aaa gat gag gta tac gtg gtg gga gcc gac tac tcc tgg   1536
165 Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp
166         500                 505                 510
168 gga ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac   1584
169 Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn
170         515                 520                 525
172 gtc atc aac gac tac ttc ctc taa                                   1608
173 Val Ile Asn Asp Tyr Phe Leu
174         530                 535
177 <210> SEQ ID NO: 2
178 <211> LENGTH: 535
179 <212> TYPE: PRT
180 <213> ORGANISM: Aplysia punctata
182 <400> SEQUENCE: 2
183 Met Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val
184 1               5                   10                  15
186 His Ala Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val
187                 20                  25                  30
189 Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly
190         35                  40                  45
192 Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
193         50                  55                  60
```

```
195 Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu
196  65              70                  75                      80
198 Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile
199              85                  90                  95
201 Glu Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu
202             100                 105                 110
204 Thr Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg
205             115                 120                 125
207 Phe Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly
208         130                 135                 140
210 Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn
211 145                 150                 155                 160
213 Leu Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly
214                 165                 170                 175
216 Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
217             180                 185                 190
219 Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
220         195                 200                 205
222 Ser Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly
223     210                 215                 220
225 Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
226 225                 230                 235                 240
228 Gly Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu
229                 245                 250                 255
231 Ser Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp
232             260                 265                 270
234 Ser Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys
235     275                 280                 285
237 Thr Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp
238     290                 295                 300
240 Gly Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala
241 305                 310                 315                 320
243 Gln Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp
244             325                 330                 335
246 Trp Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val
247     340                 345                 350
249 Arg Pro Ile Pro Ala Ser Lys Val Phe Met Ser Phe Asp Gln Pro Trp
250     355                 360                 365
252 Trp Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu
253     370                 375                 380
255 Phe Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr
256 385                 390                 395                 400
258 Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg
259             405                 410                 415
261 Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr
262         420                 425                 430
264 Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr
265         435                 440                 445
267 Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala
```

```
268      450                   455                   460
270 Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr
271 465                   470                   475                   480
273 Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg
274                   485                   490                   495
276 Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp
277              500                   505                   510
279 Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn
280         515                   520                   525
282 Val Ile Asn Asp Tyr Phe Leu
283      530                   535
287 <210> SEQ ID NO: 3
288 <211> LENGTH: 1605
289 <212> TYPE: DNA
290 <213> ORGANISM: Aplysia punctata
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(1605)
296 <400> SEQUENCE: 3
297 tcg tct gct gtg ctt ctc ctg gct tgt gcg ttg gtc atc tct gtc cac    48
298 Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val His
299  1            5                  10                  15
301 gcc gac ggt gtc tgc aga aac aga cgt caa tgt aac aga gag gtg tgc    96
302 Ala Asp Gly Val Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys
303              20                  25                  30
305 ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga gct   144
306 Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala
307         35                  40                  45
309 aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg ttc   192
310 Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
311      50                  55                  60
313 gag tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc   240
314 Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
315 65                  70                  75                  80
317 aac aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag   288
318 Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu
319                   85                  90                  95
321 ggc gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta acc   336
322 Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
323              100                 105                 110
325 ccc aag gtg ttc aag gaa ggt ttc gga aag gag ggc aga cag aga ttt   384
326 Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
327         115                 120                 125
329 tac ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg gac   432
330 Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
331      130                 135                 140
333 gta ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat ctg   480
334 Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu
335 145                 150                 155                 160
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/20/2006
PATENT APPLICATION: US/10/542,769A   TIME: 12:14:07

Input Set : **A:\WEICK046.APP**
Output Set: **N:\CRF4\03202006\J542769A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 1,3,7,9
Seq#:35; Xaa Pos. 5
Seq#:36; Xaa Pos. 6,7
Seq#:42; N Pos. 20,22,58,73,132,150,182,220,254,317,338
Seq#:43; Xaa Pos. 7,8,20,25,44,50,58,59,61,74,85,106,107,112,113,132,133
Seq#:43; Xaa Pos. 137,145
Seq#:44; Xaa Pos. 7,19,24,44,50,61,73,85,106,109,113,127,138
Seq#:45; Xaa Pos. 6,7,19,24,33,44,50,60,73,84,105,112,113,133
Seq#:46; Xaa Pos. 3
Seq#:49; Xaa Pos. 3
Seq#:51; Xaa Pos. 5
Seq#:59; N Pos. 17
Seq#:63; N Pos. 24,25,29,30,34,35
Seq#:76; Xaa Pos. 7,8
Seq#:77; Xaa Pos. 1
Seq#:78; Xaa Pos. 21,22,52,60,69,77

```
L:1251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:1445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:60
L:1446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:120
L:1447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:180
L:1448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:240
L:1449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:300
L:1530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:1533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:16
L:1536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:32
L:1539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:48
L:1542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:64
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:80
L:1548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:96
L:1551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:112
L:1554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:128
L:1557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:144
L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:1635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:16
L:1638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:32
L:1641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:48
L:1644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:64
L:1647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:80
L:1650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:96
L:1653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:112
L:1656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:128
L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:1732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:16
L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:32
L:1738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:48
L:1741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:64
L:1744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:80
L:1747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:96
L:1750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:112
L:1753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:128
L:1771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
L:1806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:1831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:2014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0
L:2205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
L:2220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:0
L:2258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:16
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:48
L:2267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:64
```